SEQUENCE LISTING

<110>   University of Florida Research Foundation, Inc.
        Hannah, L. Curtis
        Lyerly Linebarger, Carla R.

<120>   Heat Stable Variants of Adenosine Diphosphate Glucose
        Pyrophosphorylase

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<141>   2006-10-10

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Asp Ser Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile
        35                  40                  45

Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys
    50                  55                  60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp
65                  70                  75                  80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val
                85                  90                  95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala
            100                 105                 110

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val
        115                 120                 125

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr
    130                 135                 140

Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val
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Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr
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Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val
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Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met
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Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys
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Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu
225   230   235   240

Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile
                245   250   255

Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe
                260   265   270

Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser
                275   280   285

Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp
        290   295   300

Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys
305   310   315   320

Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr
                325   330   335

Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp Val
                340   345   350

Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys Ile
                355   360   365

Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala Ile
        370   375   380

Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu Ala
385   390   395   400

Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile Gly
                405   410   415

Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile
                420   425   430

Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala Ala
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cgtgcaactg catttggcct catgaaaatt gatgaagaag ggaggatcat tgagtttgct     660

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            20   25   30

Asp Ser Thr Cys Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile
        35   40   45

Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys
    50   55   60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp
65   70   75   80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val
                85   90   95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala
            100   105   110

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val
        115   120   125

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr
    130   135   140

Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val
145   150   155   160

Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr
                165   170   175

Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val
            180   185   190

Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met
        195   200   205

Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys
    210   215   220

Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu
225   230   235   240

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Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile
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Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe
              260               265               270

Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser
          275               280               285

Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp
      290               295               300

Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys
305               310               315               320

Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr
              325               330               335

Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp Val
          340               345               350

Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys Ile
          355               360               365

Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala Ile
      370               375               380

Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu Ala
385               390               395               400

Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile Gly
              405               410               415

Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile
          420               425               430

Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala Ala
          435               440               445

Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val Ile
      450               455               460

Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile
465               470               475
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Asp Ser Gln Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly
        35                  40                  45

Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys
    50                  55                  60

Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile
65                  70                  75                  80

Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr
                85                  90                  95

Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg
            100                 105                 110

Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu
            115                 120                 125

Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly
130                 135                 140

Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn
145                 150                 155                 160

Val Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp
                165                 170                 175

Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr
            180                 185                 190

Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu
            195                 200                 205

Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro
    210                 215                 220

Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly
225                 230                 235                 240

Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly
                245                 250                 255

Ile Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln
            260                 265                 270

Phe Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr
        275                 280                 285

Ser Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu
    290                 295                 300

Asp Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr
305                 310                 315                 320

Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile
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Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp
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Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys
            355                      360                      365

Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala
    370                      375                      380

Ile Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu
385                      390                      395                      400

Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile
            405                      410                      415

Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg
            420                      425                      430

Ile Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala
            435                      440                      445

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cccttgacaa agaagcgtgc caagcctgca gtgccattgg gtgccaacta tagactgatt    240

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aaacgtgcaa ctgcatttgg cctcatgaaa attgatgaag aagggaggat cattgagttt    660
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            20                  25                  30

Asp Ser Gln Thr Cys Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly
        35                  40                  45

Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys
    50                  55                  60

Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile
65                  70                  75                  80

Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr
                85                  90                  95

Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg
            100                 105                 110

Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu
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        115                    120                    125

Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly
    130                    135                    140

Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn
145                    150                    155                    160

Val Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp
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Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr
            180                    185                    190

Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu
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Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro
    210                    215                    220

Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly
225                    230                    235                    240

Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly
            245                    250                    255

Ile Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln
    260                    265                    270

Phe Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr
    275                    280                    285

Ser Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu
    290                    295                    300

Asp Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr
305                    310                    315                    320

Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile
            325                    330                    335

Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp
            340                    345                    350

Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys
    355                    360                    365

Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala
    370                    375                    380

Ile Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu
385                    390                    395                    400

Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile
            405                    410                    415

Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg
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             420                 425                 430
Ile Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala
         435                 440                 445

Ala Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val
     450                 455                 460

Ile Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile
465                 470                 475
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gtgatggaat ttctaattct tgctggcgat cacctgtacc ggatggacta tgaaaagttc       540

attcaggcac acagagaaac aaatgctgat attaccgttg ctgccctacc gatggatgag       600

aaacgtgcaa ctgcatttgg cctcatgaaa attgatgaag aagggaggat cattgagttt       660

gctgagaaac cgaaaggaga gcagttgaaa gcaatgatgg ttgacaccac catacttggc       720

cttgatgacg tgagggcaaa ggaaatgcct tatattgcta gcatgggtat ctatgttttc       780

agcaaagatg taatgcttca gctcctccgt gaacaatttc ctgaagccaa tgactttgga       840

agtgaggtta ttccaggtgc aaccagcatt ggaaagaggg ttcaggctta tctgtatgat       900

ggttactggg aagatatcgg taccattgcg gcattttata atgcaaactt gggaataacc       960

aagaagccaa taccagattt cagcttctat gaccgtttg ctccaattta tacacaacct      1020

cgacacctgc caccttcaaa ggttcttgat gctgatgtga cagacagtgt tattggtgaa      1080

ggatgtgtta ttaaaaactg caagatanac cattctgtag ttggactccg atcttgcata      1140

tctgaaggtg ctatcataga ggacagttta ctaatgggtg cggactacta tgagacagaa      1200
```

```
gctgataaaa aactccttgc cgaaaaaggt ggcattccta ttggtattgg gaaaaattca    1260

tgcatcagga gagcaatcat tgacaagaat gctcgaattg gagacaatgt taagatactc    1320

aatgctgaca atgttcaaga agctgcaatg gagacagacg ggtacttcat caaaggtgga    1380

attgtcacag tgatcaagga tgctttactc cctagtggaa cagttata               1428
```

<210>   10
<211>   476
<212>   PRT
<213>   zea mays

<400>   10

```
Met Asp Met Ala Leu Ala Ser Lys Ala Ser Pro Pro Pro Trp Asn Ala
1                5                  10                  15

Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn
            20                  25                  30

Asp Ser Glu Thr Cys Leu Asn Pro Gln His Asp Ser Val Leu Gly
            35                  40                  45

Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys
        50                  55                  60

Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile
65                  70                  75                  80

Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr
                85                  90                  95

Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg
            100                 105                 110

Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu
        115                 120                 125

Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly
        130                 135                 140

Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn
145                 150                 155                 160

Val Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp
            165                 170                 175

Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr
        180                 185                 190

Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu
        195                 200                 205

Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro
```

```
    210                   215                   220

Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly
225                   230                   235                   240

Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly
                  245                   250                   255

Ile Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln
                  260                   265                   270

Phe Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr
                  275                   280                   285

Ser Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu
    290                   295                   300

Asp Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr
305                   310                   315                   320

Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile
                  325                   330                   335

Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp
                  340                   345                   350

Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys
              355                   360                   365

Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala
    370                   375                   380

Ile Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu
385                   390                   395                   400

Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile
                  405                   410                   415

Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg
              420                   425                   430

Ile Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala
    435                   440                   445

Ala Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val
    450                   455                   460

Ile Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile
465                   470                   475
```

<210> 11
<211> 1582
<212> DNA
<213> Zea mays

<220>

```
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1578)
<223> k = g or t.

<400> 11
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac  51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
           1               5                  10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta   99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15              20                  25                  30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt  147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                 35                  40                  45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct  195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
             50                  55                  60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat  243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
         65                  70                  75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga  291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
     80                  85                  90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct  339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95                 100                 105                 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc  387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
             115                 120                 125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act  435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
             130                 135                 140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac  483
```

```
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
        145                     150                     155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa    531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
    160                     165                     170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt    579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175                     180                     185                 190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att    627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
                    195                     200                 205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt    675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
                210                     215                 220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct    723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
            225                     230                 235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat    771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
    240                     245                 250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat    819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255                     260                 265                 270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat    867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
                275                     280                 285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc    915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
                290                     295                 300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta    963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
            305                     310                 315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cat agt   1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser
        320                     325                 330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc   1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335                     340                 345                 350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag   1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
                355                     360                 365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc   1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
```

```
          370                 375                 380
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc   1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
        385                 390                 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att   1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
        400                 405                 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg   1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415                 420                 425                 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta   1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
                435                 440                 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata   1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
            450                 455                 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg   1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
            465                 470                 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg   1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
        480                 485                 490

tac tcg tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca   1539
Tyr Ser Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala
495                 500                 505                 510

acc atc aac gat ggg tct gtc ata tagatcggct gcgtktgcg             1582
Thr Ile Asn Asp Gly Ser Val Ile
                515
```

```
<210> 12
<211> 518
<212> PRT
<213> Zea mays

<400> 12

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
  1               5                  10                  15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
             20                  25                  30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
        35                  40                  45

Arg Val Ala Ala Thr Thr Gln Ile Cys Ile Leu Thr Ser Asp Ala Cys Pro
    50                  55                  60
```

```
Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65                  70              75                  80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
             85                  90                  95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
            100                 105             110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
        115                 120             125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
130                 135             140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145                 150             155             160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
            165             170                 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
        180             185             190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
        195             200             205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
        210             215             220

Lys His Val Glu Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225                 230             235             240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
            245                 250             255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
        260             265             270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
        275             280             285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
        290             295             300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305                 310             315             320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln
            325             330             335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
        340             345             350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
        355             360             365
```

```
Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
    370             375             380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
385             390             395             400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
            405             410             415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
            420             425             430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
        435             440             445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
    450             455             460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465             470             475             480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Ser
            485             490             495

Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
        500             505             510

Asn Asp Gly Ser Val Ile
        515
```

```
<210> 13
<211> 1582
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.
```

<220>
<221> variation
<222> (1578)
<223> k = g or t.

<400> 13
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
          1   5   10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta   99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15   20   25   30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt   147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                35   40   45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct   195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
        50   55   60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat   243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
 65   70   75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga   291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
 80   85   90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct   339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95   100   105   110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc   387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
                115   120   125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act   435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
                130   135   140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac   483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
        145   150   155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa   531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
 160   165   170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt   579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
 175   180   185   190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att   627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile

```
                195                    200                    205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt   675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
                210                    215                    220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct   723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
                225                    230                    235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat   771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
                240                    245                    250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat   819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255                    260                    265                    270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat   867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
                275                    280                    285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc   915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
                290                    295                    300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta   963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
                305                    310                    315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt   1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser
320                    325                    330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc   1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335                    340                    345                    350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag   1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
                355                    360                    365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc   1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
                370                    375                    380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc   1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
                385                    390                    395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att   1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
                400                    405                    410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg   1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415                    420                    425                    430
```

```
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta    1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
              435                 440                 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata    1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
          450                 455                 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg    1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
          465                 470                 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg    1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
      480                 485                 490

tac tcg tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca    1539
Tyr Ser Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala
495                 500                 505                 510

acc atc aac gat ggg tct gtc ata tagatcggct gcgtktgcg              1582
Thr Ile Asn Asp Gly Ser Val Ile
              515
```

<210> 14
<211> 518
<212> PRT
<213> Zea mays

<400> 14

```
Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
  1               5                  10                  15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
             20                  25                  30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
         35                  40                  45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
     50                  55                  60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65                  70                  75                  80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
                 85                  90                  95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
             100                 105                 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
         115                 120                 125
```

```
Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
    130                     135                 140
```

```
Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145                 150                 155                 160
```

```
Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
                165                 170                 175
```

```
Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
            180                 185                 190
```

```
Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
        195                 200                 205
```

```
Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
    210                 215                 220
```

```
Lys His Val Glu Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225                 230                 235                 240
```

```
Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
                245                 250                 255
```

```
Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
            260                 265                 270
```

```
Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
        275                 280                 285
```

```
Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
    290                 295                 300
```

```
Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305                 310                 315                 320
```

```
Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln
                325                 330                 335
```

```
Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
            340                 345                 350
```

```
Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
        355                 360                 365
```

```
Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
    370                 375                 380
```

```
Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
385                 390                 395                 400
```

```
Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
                405                 410                 415
```

```
Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
            420                 425                 430
```

```
Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
        435                 440                 445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
    450                 455                 460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465                 470                 475                 480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Ser
                485                 490                 495

Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
        500                 505                 510

Asn Asp Gly Ser Val Ile
        515
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<210> 15
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1572)
<223> k = g or t.

<400> 15
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
          1               5                   10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta   99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
```

```
 15                    20                    25                        30
agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt        147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
               35                    40                    45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct       195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
               50                    55                    60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat       243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
               65                    70                    75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga       291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
               80                    85                    90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct       339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95                   100                   105                   110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc       387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
               115                   120                   125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act       435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
               130                   135                   140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac       483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
               145                   150                   155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa       531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
               160                   165                   170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt       579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175                   180                   185                   190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att       627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
               195                   200                   205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt       675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
               210                   215                   220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct       723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
               225                   230                   235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat       771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
               240                   245                   250
```

```
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat    819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255                     260                 265                 270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat    867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
                    275                 280                 285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc    915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
                290                 295                 300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta    963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
            305                 310                 315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt   1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser
320                 325                 330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc   1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335                 340                 345                 350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag   1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
                355                 360                 365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc   1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
                370                 375                 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc   1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
            385                 390                 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att   1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
400                 405                 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg   1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415                 420                 425                 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta   1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
                435                 440                 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata   1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
            450                 455                 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg   1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
            465                 470                 475
```

```
atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg    1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
    480                     485                 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc    1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495                     500                 505                 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg                       1576
Asn Asp Gly Ser Val Ile
                    515
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<210> 16
<211> 516
<212> PRT
<213> Zea mays

<400> 16

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
1               5                   10                  15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
            20                  25                  30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
        35                  40                  45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
    50                  55                  60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
65                  70                  75                  80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
                85                  90                  95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
            100                 105                 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
        115                 120                 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
    130                 135                 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145                 150                 155                 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
                165                 170                 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
            180                 185                 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
```

```
          195                    200                     205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
    210                    215                    220

Lys His Val Glu Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225                    230                    235                240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
                245                    250                    255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
        260                    265                    270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
        275                    280                    285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
    290                    295                    300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305                    310                    315                320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln
                325                    330                    335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
            340                    345                    350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
        355                    360                    365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
    370                    375                    380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
385                    390                    395                400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
            405                    410                    415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
        420                    425                    430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu Leu Leu
        435                    440                    445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
    450                    455                    460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465                    470                    475                480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
            485                    490                    495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
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              500              505              510
Gly Ser Val Ile
        515


<210> 17
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (540)
<223> n = a or g or c or t/u, unknown, or other.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1572)
<223> k = g or t.

<400> 17
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
          1               5                   10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
15              20                  25                  30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
            35                  40                  45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
```

```
                50                    55                    60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat   243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
            65                    70                    75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga   291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
        80                    85                    90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct   339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
    95                    100                   105                   110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc   387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
                115                   120                   125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act   435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
            130                   135                   140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac   483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
            145                   150                   155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa   531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
        160                   165                   170

gag cca ccn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt   579
Glu Pro Pro Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175                   180                   185                   190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att   627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
                195                   200                   205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt   675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
            210                   215                   220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct   723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
                225                   230                   235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat   771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
        240                   245                   250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat   819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255                   260                   265                   270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat   867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
                275                   280                   285
```

```
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc    915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
            290                     295                     300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta    963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
            305                     310                     315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt   1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser
        320                     325                     330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc   1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335                     340                     345                 350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag   1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
                    355                     360                 365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc   1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
            370                     375                     380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc   1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
                385                     390                     395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att   1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
400                     405                     410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg   1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415                     420                     425                 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta   1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
                    435                     440                 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata   1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
            450                     455                     460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg   1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
        465                     470                     475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg   1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
        480                     485                     490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc   1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495                     500                     505                 510
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aac gat ggg tct gtc ata tagatcggct gcgtktgcg                          1576
Asn Asp Gly Ser Val Ile
            515
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<210> 18
<211> 516
<212> PRT
<213> Zea mays

<400> 18

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
 1               5                   10                  15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
            20                  25                  30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
            35                  40                  45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
    50                  55                  60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65                  70                  75                  80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
                85                  90                  95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
            100                 105                 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
            115                 120                 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
            130                 135                 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145                 150                 155                 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
                165                 170                 175

Pro Gly Trp Phe Gln Gly Thr Ala Gln Ser Ile Arg Lys Phe Ile Trp
            180                 185                 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
            195                 200                 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
    210                 215                 220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225                 230                 235                 240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
```

```
              245                 250                 255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
            260                 265                 270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
            275                 280                 285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
        290                 295                 300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305                 310                 315                 320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln
            325                 330                 335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
            340                 345                 350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
            355                 360                 365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
        370                 375                 380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
385                 390                 395                 400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
            405                 410                 415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
            420                 425                 430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
            435                 440                 445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
        450                 455                 460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465                 470                 475                 480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
            485                 490                 495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
        500                 505                 510

Gly Ser Val Ile
        515
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<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1209)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1371)
<223> h = a or c or t/u.

<220>
<221> variation
<222> (1572)
<223> k = g or t.

<400> 19
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
           1   5   10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta   99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15   20   25   30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt   147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                 35   40   45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct   195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
             50   55   60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat   243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr

```
         65                    70                   75
gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga   291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
        80                    85                   90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct   339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95                    100                  105                110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc   387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
               115                  120                  125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act   435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
           130                  135                  140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac   483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
           145                  150                  155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa   531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
       160                  165                  170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt   579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175                  180                  185                  190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att   627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
               195                  200                  205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt   675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
           210                  215                  220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct   723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
           225                  230                  235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat   771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
       240                  245                  250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat   819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255                  260                  265                  270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat   867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
               275                  280                  285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc   915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
           290                  295                  300
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aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta     963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
        305                 310                 315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt    1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser
        320                 325                 330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc    1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335                 340                 345                 350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag    1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
                355                 360                 365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc    1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
                370                 375                 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc    1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
                385                 390                 395

tca cay ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att    1251
Ser His Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
        400                 405                 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg    1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415                 420                 425                 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta    1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
                435                 440                 445

ctg tta gct ggg aag gtc ccr ath gga ata gga agg aac aca aag ata    1395
Leu Leu Ala Gly Lys Val Pro Ile Gly Ile Gly Arg Asn Thr Lys Ile
            450                 455                 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg    1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
            465                 470                 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg    1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
        480                 485                 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc    1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495                 500                 505                 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg                       1576
Asn Asp Gly Ser Val Ile
        515
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<210> 20
<211> 516
<212> PRT
<213> Zea mays

<400> 20

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
 1   5   10   15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
            20   25   30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
        35   40   45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
    50   55   60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
65   70   75   80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
                85   90   95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
        100   105   110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
        115   120   125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
    130   135   140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145   150   155   160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
                165   170   175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
        180   185   190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
        195   200   205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
    210   215   220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225   230   235   240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
                245   250   255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn

```
                  260                    265                    270
Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
            275                    280                    285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
        290                    295                    300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305                    310                    315                    320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln
                    325                    330                    335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
            340                    345                    350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
            355                    360                    365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
370                    375                    380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser His
385                    390                    395                    400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
                    405                    410                    415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
            420                    425                    430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu Leu Leu
            435                    440                    445

Ala Gly Lys Val Pro Ile Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
        450                    455                    460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465                    470                    475                    480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
                    485                    490                    495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
            500                    505                    510

Gly Ser Val Ile
            515
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<210> 21
<211> 1576
<212> DNA
<213> Zea mays

<220>

<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (321)
<223> n = a or g or c or t/u, unknown, or other.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1572)
<223> k = g or t.

<400> 21
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac   51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
           1   5   10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta   99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15   20   25   30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
              35   40   45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
          50   55   60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
      65   70   75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
  80   85   90

tct cag ctc ttt cct ctg aca agc aca acn gct acg cct gct gta cct 339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Thr Ala Thr Pro Ala Val Pro

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 95                    100                   105                   110
gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc    387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
                115               120               125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act    435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
            130               135               140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac    483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
            145               150               155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa    531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
        160               165               170

gag cca gct gga tgg ttc cag ggt aca gca gca tct atc aga aaa ttt    579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Ala Ser Ile Arg Lys Phe
175               180               185               190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att    627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
            195               200               205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt    675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
            210               215               220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct    723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
            225               230               235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat    771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
        240               245               250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat    819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
        255               260               265               270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat    867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
                275               280               285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc    915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
            290               295               300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta    963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
            305               310               315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt   1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser
            320               325               330
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gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc   1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335                 340                 345                 350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag   1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
                    355                 360                 365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc   1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
                370                 375                 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc   1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
            385                 390                 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att   1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
        400                 405                 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg   1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
    415                 420                 425                 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta   1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
                    435                 440                 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata   1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
                450                 455                 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg   1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
            465                 470                 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg   1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
        480                 485                 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc   1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
    495                 500                 505                 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg                      1576
Asn Asp Gly Ser Val Ile
                515
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<210> 22
<211> 516
<212> PRT
<213> Zea mays

<400> 22
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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
 1               5                  10                 15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
            20                  25                 30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
        35                  40                  45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
    50                  55                  60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65                 70                  75                 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
                85                  90                  95

Leu Phe Pro Leu Thr Ser Thr Thr Ala Thr Pro Ala Val Pro Val Gly
        100                 105                 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
        115                 120                 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
    130                 135                 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145                 150                 155                 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
            165                 170                 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
        180                 185                 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
        195                 200                 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
    210                 215                 220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225                 230                 235                 240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
            245                 250                 255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
        260                 265                 270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
        275                 280                 285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
    290                 295                 300
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Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305                 310                 315                 320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln
                325                 330                 335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
                340                 345                 350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
                355                 360                 365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
        370                 375                 380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
385                 390                 395                 400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
                405                 410                 415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
                420                 425                 430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
        435                 440                 445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
        450                 455                 460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465                 470                 475                 480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
                485                 490                 495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
                500                 505                 510

Gly Ser Val Ile
        515
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<210> 23
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
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<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1389)
<223> h = a or c or t/u.

<220>
<221> variation
<222> (1572)
<223> k = g or t.

<400> 23
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ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac   51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
            1               5                  10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta     99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15              20                  25                  30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt    147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
            35                  40                  45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct    195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
        50                  55                  60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat    243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
        65                  70                  75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga    291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
    80                  85                  90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct    339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95                  100                 105                 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc    387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
            115                 120                 125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act    435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
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                130                      135                   140
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac    483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
            145                      150                   155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa    531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
        160                      165                   170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt    579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
    175                      180                   185             190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att    627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
                195                      200                   205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt    675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
            210                      215                   220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct    723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
            225                      230                   235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat    771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
        240                      245                   250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat    819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
    255                      260                   265             270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat    867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
                275                      280                   285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc    915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
        290                      295                   300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta    963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
            305                      310                   315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt    1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser
    320                      325                   330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc    1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335                      340                   345                   350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag    1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
            355                      360                   365
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ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc    1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
            370                 375                 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc    1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
        385                 390                 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att    1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
        400                 405                 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg    1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415                 420                 425                 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta    1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
                435                 440                 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac ath aag ata    1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Ile Lys Ile
                450                 455                 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg    1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
            465                 470                 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg aag gaa ggg    1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
        480                 485                 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc    1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495                 500                 505                 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg                       1576
Asn Asp Gly Ser Val Ile
                515
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<210> 24
<211> 516
<212> PRT
<213> Zea mays

<400> 24

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
  1               5                   10                  15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
            20                  25                  30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
            35                  40                  45
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Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
    50   55   60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65   70   75   80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
                    85   90   95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
                100   105   110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
            115   120   125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
        130   135   140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145   150   155   160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
                165   170   175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
            180   185   190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
        195   200   205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
        210   215   220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225   230   235   240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
                245   250   255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
        260   265   270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
        275   280   285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
    290   295   300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305   310   315   320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln
                325   330   335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
            340   345   350

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Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
        355                 360                 365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
    370                 375                 380

Pro Thr Gln Leu Asp Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
385                 390                 395                 400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
            405                 410                 415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
            420                 425                 430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
        435                 440                 445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Ile Lys Ile Arg Asn
    450                 455                 460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465                 470                 475                 480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
            485                 490                 495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
            500                 505                 510

Gly Ser Val Ile
        515
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<210> 25
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (657)
<223> n = a or g or c or t/u, unknown, or other.

<220>
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<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1572)
<223> k = g or t.

<400> 25
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
          1               5                   10


cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
15                  20                  25                  30


agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                35                  40                  45


ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
            50                  55                  60


tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
        65                  70                  75


gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
        80                  85                  90


tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
95                  100                 105                 110


gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
                115                 120                 125


aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
                130                 135                 140


tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
            145                 150                 155


ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
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     160                     165                   170
gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt    579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175                     180                   185                   190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att    627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
                        195                   200                   205

gta atc ttg agt ggc gat cag ctt tat ccn atg aat tac atg gaa ctt    675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Pro Met Asn Tyr Met Glu Leu
             210                   215                   220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct    723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
             225                   230                   235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat    771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
240                     245                   250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat    819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255                     260                   265                   270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat    867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
                        275                   280                   285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc    915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
             290                   295                   300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta    963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
             305                   310                   315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt    1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser
320                     325                   330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc    1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335                     340                   345                   350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag    1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
                        355                   360                   365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc    1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
             370                   375                   380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc    1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
             385                   390                   395
```

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tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att   1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
    400                     405                 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg   1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415                 420                 425                 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta   1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
                435                 440                 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata   1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
            450                 455                 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg   1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
        465                 470                 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg   1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
    480                 485                 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc   1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495                 500                 505                 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg                      1576
Asn Asp Gly Ser Val Ile
                515


<210> 26
<211> 516
<212> PRT
<213> Zea mays

<400> 26

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
 1               5                   10                  15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
            20                  25                  30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
        35                  40                  45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
    50                  55                  60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65                 70                  75                  80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
```

```
                        85                    90                        95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
            100                     105                 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
            115                     120                 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
        130                     135                 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145                     150                     155                 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
                165                     170                 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
            180                     185                 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
        195                     200                 205

Leu Ser Gly Asp Gln Leu Tyr Pro Met Asn Tyr Met Glu Leu Val Gln
        210                     215                 220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225                     230                     235                 240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
                245                     250                 255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
            260                     265                 270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
            275                     280                 285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
        290                     295                 300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305                     310                     315                 320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln
                325                     330                 335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
            340                     345                 350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
        355                     360                 365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
        370                     375                 380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
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385   390   395   400
Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
                405   410   415

Cys Ser Arg Val Ser Ser Gly Cys Leu Lys Asp Ser Val Met Met
            420   425   430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
        435   440   445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
    450   455   460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465   470   475   480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
                485   490   495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
        500   505   510

Gly Ser Val Ile
        515

<210> 27
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (540)
<223> n = a or g or c or t/u, unknown, or other.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1287)
<223> y = c or t.

<220>
<221> variation

<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1572)
<223> k = g or t.

<400> 27
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ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
           1               5                  10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta   99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15              20                  25                  30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt  147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
            35                  40                  45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct  195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
        50                  55                  60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat  243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
            65                  70                  75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga  291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
     80                  85                  90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct  339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95              100                 105                 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc  387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
            115                 120                 125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act  435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
            130                 135                 140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac  483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
            145                 150                 155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa  531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
        160                 165                 170
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gag cca gtn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt      579
Glu Pro Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175                     180                 185                 190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att      627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
                195                 200                 205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt      675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
            210                 215                 220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct      723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
        225                 230                 235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat      771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
    240                 245                 250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat      819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255                 260                 265                 270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat      867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
                275                 280                 285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc      915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
            290                 295                 300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta      963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
        305                 310                 315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt      1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser
        320                 325                 330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc      1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335                 340                 345                 350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag      1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
                355                 360                 365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc      1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
            370                 375                 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc      1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
        385                 390                 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att      1251
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```
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
    400                     405                     410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa tty aag gac tcc gtg   1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Phe Lys Asp Ser Val
415                     420                     425                     430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta   1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
                435                     440                     445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata   1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
                450                     455                     460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg   1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
            465                     470                     475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg   1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
        480                     485                     490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc   1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495                     500                     505                     510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg                       1576
Asn Asp Gly Ser Val Ile
                515
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<210> 28
<211> 516
<212> PRT
<213> Zea mays

<400> 28

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
1               5                   10                  15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
            20                  25                  30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
        35                  40                  45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
    50                  55                  60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
65                  70                  75                  80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
                85                  90                  95
```

```
Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
            100                     105                 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
            115                 120             125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
        130                 135             140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145                 150                 155                 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
                165                 170                 175

Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
            180                 185                 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
        195                 200                 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
        210                 215                 220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225                 230                 235                 240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
                245                 250                 255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
            260                 265                 270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
        275                 280                 285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
        290                 295                 300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305                 310                 315                 320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln
                325                 330                 335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
            340                 345                 350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
        355                 360                 365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
    370                 375                 380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
385                 390                 395                 400
```

```
Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
                405                 410                 415

Cys Ser Arg Val Ser Ser Gly Cys Glu Phe Lys Asp Ser Val Met Met
            420                 425                 430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
        435                 440                 445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
    450                 455                 460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465                 470                 475                 480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
                485                 490                 495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
            500                 505                 510

Gly Ser Val Ile
        515
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<210> 29
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (981)
<223> r = g or a.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1086)
<223> n = a or g or c or t/u, unknown, or other.

<220>
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<221> variation
<222> (1197)
<223> n = a or g or c or t/u, unknown, or other.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1572)
<223> k = g or t.

<400> 29
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac  51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
           1               5                  10


cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta   99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15               20                  25                  30


agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt  147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
              35                  40                  45


ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct  195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
      50                  55                  60


tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat  243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
      65                  70                  75


gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga  291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
      80                  85                  90


tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct  339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95               100                 105                 110


gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc  387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
             115                 120                 125


aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act  435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
             130                 135                 140


tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac  483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
             145                 150                 155


ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa  531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
```

```
     160                   165                   170
gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt    579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175                 180                 185                 190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att    627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
            195                 200                 205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt    675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
        210                 215                 220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct    723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
        225                 230                 235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat    771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
    240                 245                 250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat    819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
    255                 260                 265                 270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat    867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
                275                 280                 285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc    915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
            290                 295                 300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta    963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
        305                 310                 315

cat gac ttt gga tct aar atc ctc cca aga gct gta cta gat cay agt   1011
His Asp Phe Gly Ser Lys Ile Leu Pro Arg Ala Val Leu Asp His Ser
    320                 325                 330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc   1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335                 340                 345                 350

aaa tca ttc ttt gat gca aac ttg gtn ctc act gag cag cct tcc aag   1107
Lys Ser Phe Phe Asp Ala Asn Leu Val Leu Thr Glu Gln Pro Ser Lys
                355                 360                 365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc   1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
            370                 375                 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gtn ttt atc   1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile
        385                 390                 395
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tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att   1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
    400                     405                 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg   1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415                 420                 425                 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta   1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
                435                 440                 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata   1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
                450                 455                 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg   1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
            465                 470                 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg   1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
            480                 485                 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc   1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495                 500                 505                 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg                      1576
Asn Asp Gly Ser Val Ile
                515
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<210> 30
<211> 516
<212> PRT
<213> Zea mays

<400> 30

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
  1               5                  10                  15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
               20                  25                  30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
            35                  40                  45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
         50                  55                  60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65                  70                  75                  80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
```

```
                    85                  90                      95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
            100                 105                 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
            115                 120                 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
    130                 135                 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145                 150                 155                 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
            165                 170                 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
            180                 185                 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
            195                 200                 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
            210                 215                 220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225                 230                 235                 240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
            245                 250                 255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
            260                 265                 270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
    275                 280                 285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
    290                 295                 300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305                 310                 315                 320

Phe Gly Ser Lys Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln
            325                 330                 335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
            340                 345                 350

Phe Phe Asp Ala Asn Leu Val Leu Thr Glu Gln Pro Ser Lys Phe Asp
            355                 360                 365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
    370                 375                 380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp
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385   390   395   400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
                 405   410   415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
             420   425   430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
         435   440   445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
     450   455   460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465   470   475   480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
             485   490   495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
         500   505   510

Gly Ser Val Ile
         515

<210> 31
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1572)
<223> k = g or t.

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<400> 31

ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
           1               5                  10


cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta     99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15              20                  25                  30


agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt    147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
            35                  40                  45


ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct    195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
        50                  55                  60


tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat    243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
        65                  70                  75


gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga    291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
        80                  85                  90


tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct    339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95                 100                 105                 110


gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc    387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
                115                 120                 125


aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act    435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
            130                 135                 140


tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac    483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
        145                 150                 155


ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa    531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
        160                 165                 170


gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt    579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175                 180                 185                 190


atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att    627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
                195                 200                 205


gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt    675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
            210                 215                 220
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gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct    723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
            225                 230                 235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat    771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
        240                 245                 250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat    819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255                 260                 265                 270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat    867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
                275                 280                 285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc    915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
                290                 295                 300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta    963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
305                 310                 315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tty agt   1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Phe Ser
320                 325                 330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc   1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335                 340                 345                 350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag   1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
                355                 360                 365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc   1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
                370                 375                 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc   1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
                385                 390                 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att   1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
400                 405                 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg   1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415                 420                 425                 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta   1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
                435                 440                 445
```

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ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata   1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
            450                 455                 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg   1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
            465                 470                 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg   1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
            480                 485                 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc   1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495                 500                 505                 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg                      1576
Asn Asp Gly Ser Val Ile
            515
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<210> 32
<211> 516
<212> PRT
<213> Zea mays

<400> 32

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
 1               5                  10                  15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
            20                  25                  30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
            35                  40                  45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
 50                  55                  60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65                  70                  75                  80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
                    85                  90                  95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
            100                 105                 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
            115                 120                 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
            130                 135                 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145                 150                 155                 160
```

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
            165   170   175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
            180   185   190

Val Leu Glu Asp Tyr Tyr Ser Asp His Lys Ser Ile Asp Asn Ile Val Ile
            195   200   205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
    210   215   220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225   230   235   240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
            245   250   255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
            260   265   270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
    275   280   285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
    290   295   300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305   310   315   320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Phe Ser Val Gln
            325   330   335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
            340   345   350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
            355   360   365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
    370   375   380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
385   390   395   400

Gly Cys Leu Leu Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
            405   410   415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
            420   425   430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu Leu Leu
    435   440   445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
    450   455   460

```
Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465                 470                 475                 480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
                485                 490                 495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
            500                 505                 510

Gly Ser Val Ile
            515
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<210> 33
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1572)
<223> k = g or t.

<400> 33

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ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac   51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
          1                 5                  10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta   99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
15                  20                  25                  30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt  147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                35                  40                  45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct  195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
            50                  55                  60
```

```
tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat      243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
         65                  70                  75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga      291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
    80                  85                  90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct      339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95                 100                 105                 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc      387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
            115                 120                 125

aac agt ggt ata aat aag ata ttt gtg gat agt cag ttc aat tct act      435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
            130                 135                 140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac      483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
            145                 150                 155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa      531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
    160                 165                 170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt      579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175                 180                 185                 190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att      627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
            195                 200                 205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt      675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
            210                 215                 220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct      723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
            225                 230                 235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat      771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
    240                 245                 250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat      819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255                 260                 265                 270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat      867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
            275                 280                 285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc      915
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Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
            290                         295                 300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta    963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
            305                 310                 315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat atg agt   1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Met Ser
        320                 325                 330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc   1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335                 340                 345                 350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag   1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
                355                 360                 365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc   1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
        370                 375                 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc   1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
            385                 390                 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att   1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
        400                 405                 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg   1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415                 420                 425                 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta   1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
                435                 440                 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata   1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
            450                 455                 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg   1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
        465                 470                 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg   1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
        480                 485                 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc   1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495                 500                 505                 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg                      1576
Asn Asp Gly Ser Val Ile
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515

<210> 34
<211> 516
<212> PRT
<213> Zea mays

<400> 34

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
1   5   10   15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
            20   25   30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
        35   40   45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
    50   55   60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
65   70   75   80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
                85   90   95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
            100   105   110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
        115   120   125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
    130   135   140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145   150   155   160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
                165   170   175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
            180   185   190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
        195   200   205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
    210   215   220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225   230   235   240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
                245   250   255

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Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
        260                 265                 270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
        275                 280                 285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
    290                 295                 300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305                 310                 315                 320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Met Ser Val Gln
                325                 330                 335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
            340                 345                 350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
        355                 360                 365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
    370                 375                 380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
385                 390                 395                 400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
            405                 410                 415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
        420                 425                 430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu Leu Leu
        435                 440                 445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
    450                 455                 460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465                 470                 475                 480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
            485                 490                 495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
        500                 505                 510

Gly Ser Val Ile
        515


<210> 35
<211> 1576
<212> DNA
<213> Zea mays
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<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (540)
<223> n = a or g or c or t/u, unknown, or other.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1572)
<223> k = g or t.

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ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
           1   5   10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta   99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15   20   25   30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                35   40   45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
            50   55   60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
        65   70   75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
    80   85   90

```
tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct    339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95                      100                 105                 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc    387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
             115                 120                 125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act    435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
             130                 135                 140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac    483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
             145                 150                 155

ttt gct gat gga tct gta cag gta tta gcg gct aca atg cct gaa        531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
         160                 165                 170

gag cca gtn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt    579
Glu Pro Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175                 180                 185                 190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att    627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
                 195                 200                 205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt    675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
             210                 215                 220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct    723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
             225                 230                 235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat    771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
         240                 245                 250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat    819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255                 260                 265                 270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat    867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
                 275                 280                 285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc    915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
             290                 295                 300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta    963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
         305                 310                 315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt   1011
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His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser
    320                 325                 330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc   1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335                 340                 345                 350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag   1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
                    355                 360                 365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc   1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
                370                 375                 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc   1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
            385                 390                 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att   1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
400                 405                 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg   1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415                 420                 425                 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta   1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
                435                 440                 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata   1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
            450                 455                 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg   1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
            465                 470                 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg   1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
480                 485                 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc   1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495                 500                 505                 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg                       1576
Asn Asp Gly Ser Val Ile
                515
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<210> 36
<211> 516
<212> PRT
<213> Zea mays
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<400> 36

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
  1               5                   10                  15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
             20                  25                  30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
         35                  40                  45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
     50                  55                  60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65                  70                  75                  80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
             85                  90                  95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
            100                 105                 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
        115                 120                 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
        130                 135                 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145                 150                 155                 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
                165                 170                 175

Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
            180                 185                 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
        195                 200                 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
        210                 215                 220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225                 230                 235                 240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
                245                 250                 255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
            260                 265                 270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
        275                 280                 285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
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      290                  295                  300
Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305                     310                  315                  320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln
                        325                  330                  335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
                    340                  345                  350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
            355                  360                  365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
370                  375                  380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
385                  390                  395                  400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
                    405                  410                  415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
            420                  425                  430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu Leu Leu
            435                  440                  445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
450                  455                  460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465                  470                  475                  480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
                    485                  490                  495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
            500                  505                  510

Gly Ser Val Ile
            515
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<210> 37
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
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<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1197)
<223> n = a or g or c or t/u, unknown, or other.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1572)
<223> k = g or t.

<400> 37
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
           1               5                  10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta   99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15                  20                  25                  30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt   147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                     35                  40                  45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct   195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
                 50                  55                  60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat   243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
             65                  70                  75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga   291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
         80                  85                  90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct   339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95                  100                 105                 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc   387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
                 115                 120                 125
```

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aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act    435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
            130                 135                 140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac    483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
            145                 150                 155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa    531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
    160                 165                 170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt    579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175                 180                 185                 190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att    627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
                195                 200                 205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt    675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
                210                 215                 220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct    723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
                225                 230                 235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat    771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
    240                 245                 250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat    819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255                 260                 265                 270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat    867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
                275                 280                 285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc    915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
                290                 295                 300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta    963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
            305                 310                 315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt   1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser
            320                 325                 330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc   1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335                 340                 345                 350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag   1107
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Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
            355                     360                     365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc    1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
            370                 375                 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gtn ttt atc    1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile
            385                 390                 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att    1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
        400                 405                 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg    1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415                 420                 425                 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta    1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
                435                 440                 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata    1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
            450                 455                 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg    1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
        465                 470                 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg    1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
        480                 485                 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc    1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495                 500                 505                 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg                       1576
Asn Asp Gly Ser Val Ile
                515


<210> 38
<211> 516
<212> PRT
<213> Zea mays

<400> 38

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
 1                  5                   10                  15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
            20                  25                  30
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Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
         35                  40                  45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
     50                  55                  60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65                  70                  75                  80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
                 85                  90                  95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
         100                 105                 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
         115                 120                 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
 130                 135                 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
 145                 150                 155                 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
             165                 170                 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
         180                 185                 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
         195                 200                 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
 210                 215                 220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
 225                 230                 235                 240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
             245                 250                 255

Gly Arg Val Leu Gln Phe Phe Glu Pro Lys Gly Ala Asp Leu Asn
         260                 265                 270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
         275                 280                 285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
     290                 295                 300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
 305                 310                 315                 320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln
             325                 330                 335
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Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
            340                 345                 350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
        355                 360                 365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
    370                 375                 380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp
385                 390                 395                 400

Gly Cys Leu Leu Arg Glu Cys Asn Ile His Ser Val Ile Gly Val
            405                 410                 415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
            420                 425                 430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
        435                 440                 445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
    450                 455                 460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465                 470                 475                 480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
            485                 490                 495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
        500                 505                 510

Gly Ser Val Ile
        515
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<210> 39
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (540)
<223> n = a or g or c or t/u, unknown, or other.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1197)
<223> n = a or g or c or t/u, unknown, or other.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1572)
<223> k = g or t.

<400> 39
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac   51
         Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
          1   5   10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta   99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
  15   20   25   30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt   147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
            35   40   45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct   195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
        50   55   60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat   243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
        65   70   75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga   291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
    80   85   90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct   339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
  95   100   105   110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc   387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
           115   120   125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act   435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
        130   135   140

```
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac   483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
        145                 150                 155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa   531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
    160                 165                 170

gag cca gtn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt   579
Glu Pro Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175                 180                 185                 190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att   627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
            195                 200                 205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt   675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
        210                 215                 220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct   723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
        225                 230                 235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat   771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
    240                 245                 250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat   819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255                 260                 265                 270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat   867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
            275                 280                 285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc   915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
        290                 295                 300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta   963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
        305                 310                 315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt   1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser
320                 325                 330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc   1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335                 340                 345                 350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag   1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
            355                 360                 365
```

```
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc   1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
            370                 375                 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gtn ttt atc   1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile
            385                 390                 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att   1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
    400                 405                 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg   1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415                 420                 425                 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta   1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
            435                 440                 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata   1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
            450                 455                 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg   1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
            465                 470                 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg   1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
    480                 485                 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc   1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495                 500                 505                 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg                      1576
Asn Asp Gly Ser Val Ile
            515
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<210> 40
<211> 516
<212> PRT
<213> Zea mays

<400> 40

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
  1               5                   10                  15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
            20                  25                  30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
        35                  40                  45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
```

```
       50                    55                      60
Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65                    70                    75                    80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
                      85                    90                    95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
              100                   105                   110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
              115                   120                   125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
              130                   135                   140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145                   150                   155                   160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
                      165                   170                   175

Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
              180                   185                   190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
              195                   200                   205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
210                   215                   220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225                   230                   235                   240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
              245                   250                   255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
              260                   265                   270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
              275                   280                   285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
              290                   295                   300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305                   310                   315                   320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln
                      325                   330                   335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
              340                   345                   350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
```

```
            355                    360                    365
Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
    370                    375                    380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp
385                    390                    395                    400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
                405                    410                    415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
                420                    425                    430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
                435                    440                    445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
    450                    455                    460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465                    470                    475                    480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
                485                    490                    495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
                500                    505                    510

Gly Ser Val Ile
                515
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<210> 41
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (540)
<223> n = a or g or c or t/u, unknown, or other.

<220>
<221> variation
<222> (1008)

<223> y = c or t.

<220>
<221> variation
<222> (1197)
<223> n = a or g or c or t/u, unknown, or other.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1572)
<223> k = g or t.

<400> 41
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ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac  51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
           1               5                  10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta   99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15              20                  25                      30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt  147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                35                  40                  45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct  195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
            50                  55                  60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat  243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
            65                  70                  75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga  291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
 80                  85                  90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct  339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95                  100                 105                 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc  387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
                115                 120                 125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act  435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
                130                 135                 140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac  483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
                145                 150                 155
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ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa    531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
    160                     165                 170

gag cca gtn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt    579
Glu Pro Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175                     180                 185                 190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att    627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
                    195                 200                 205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt    675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
                210                 215                 220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct    723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
            225                 230                 235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat    771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
        240                 245                 250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat    819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255                 260                 265                 270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat    867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
                275                 280                 285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc    915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
                290                 295                 300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta    963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
            305                 310                 315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt   1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser
320                 325                 330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc   1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335                 340                 345                 350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag   1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
                355                 360                 365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc   1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
            370                 375                 380
```

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ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gtn ttt atc   1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile
        385                 390                 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att   1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
400                 405                 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg   1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415                 420                 425                 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta   1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
                435                 440                 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata   1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
            450                 455                 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg   1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
        465                 470                 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg   1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
    480                 485                 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc   1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495                 500                 505                 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg                      1576
Asn Asp Gly Ser Val Ile
            515
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<210> 42
<211> 516
<212> PRT
<213> Zea mays

<400> 42

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
1               5                   10                  15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
            20                  25                  30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Asn Arg Cys Phe Gly Gly
        35                  40                  45

Arg Val Ala Ala Thr Thr Gln Ile Leu Thr Ser Asp Ala Cys Pro
    50                  55                  60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
```

```
65                      70                   75                      80
Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
                    85                   90                   95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
                100                  105                  110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
        115                  120                  125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
    130                  135                  140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145                  150                  155                  160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
                165                  170                  175

Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
            180                  185                  190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
        195                  200                  205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
    210                  215                  220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225                  230                  235                  240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
                245                  250                  255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
            260                  265                  270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
        275                  280                  285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
    290                  295                  300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305                  310                  315                  320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln
            325                  330                  335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
        340                  345                  350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
    355                  360                  365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
```

```
    370                      375                    380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp
385                      390                  395                    400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
                    405                      410                    415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
              420                    425                    430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
          435                    440                    445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
        450                    455                    460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465                      470                    475                    480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
                  485                    490                    495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
            500                    505                    510

Gly Ser Val Ile
          515
```